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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/234,733A

DATE: 05/01/2002

TIME: 13:06:29

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\05012002\1234733A.raw

3 <110> APPLICANT: JIANG, Min
4 PÖTTER, Andrew A.
5 MACLACHLAN, Philip R.
7 <120> TITLE OF INVENTION: CAMP FACTOR OF STREPTOCOCCUS UBERIS
9 <130> FILE REFERENCE: 9000-0030.10
11 <140> CURRENT APPLICATION NUMBER: 09/234,733A
12 <141> CURRENT FILING DATE: 1999-01-21
14 <160> NUMBER OF SEQ ID NOS: 5
16 <170> SOFTWARE: PatentIn Ver. 2.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1191
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial Sequence
23 <220> FEATURE:
24 <223> OTHER INFORMATION: Description of Artificial Sequence: S. uberis CAMP
25 factor gene
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (157)..(924)
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33 ttaaaaaaaat tgtaactgtat tgatacaggc ataagtactt atttatttta tagattgcaa 120
36 ttatataaaca attatatttt tcaaagagga atgctt atq gaa ttc aaa aag tta 174
37 Met Glu Phe Lys Lys Leu
38 1 5
40 ett tat tta act qqt tca atc qea qqa att act tta ttt tcc cca att 222
41 leu tyr leu thr gly ser ile ala gly ile thr leu phe ser pro ile
42 10 15 20
43 tta aca aqt qtc caa qea aat caa ata aat qtt aqt caa cca tct aat 270
45 leu thr ser val gln ala asn gln ile asn val ser gln pro ser asn
46 25 30 35
48 aat qaa aqt aat gtt att tca caq aaa aaa qaa qaa att qat aat aqt 318
49 asn glu ser asn val ile ser gln lys lys glu glu ile asp asn ser
50 40 45 50
52 eta aat caq qaa aqt qct caa cta tat qcc ttq aaa qaa qat qtt aaa 366
53 leu asn gln glu ser ala gln leu tyr ala leu lys glu asp val lys
54 55 60 65 70

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64	aat	tct	att	gga	aca	aga	gta	gaa	qca	atc	tct	gac	gtg	att	caa	gca	510
65	Asn	Ser	Ile	Gly	Thr	Arg	Val	Glu	Ala	Ile	Ser	Asp	Val	Ile	Gln	Ala	
66			105				110				115						
68	att	gtt	ttt	tca	acq	caa	cag	tta	aca	aat	aaa	gtt	gat	caa	qct	cac	558
69	Ile	Val	Phe	Ser	Thr	Gln	Gln	Leu	Thr	Asn	Lys	Val	Asp	Gln	Ala	His	
70			120				125				130						
72	att	gtt	atq	gga	ttt	qct	att	acq	aaa	tta	ctt	att	cgc	att	qca	gac	606
73	Ile	Asp	Met	Gly	Phe	Ala	Ile	Thr	Lys	Leu	Leu	Ile	Arg	Ile	Ala	Asp	
74			135				140				145				150		
76	cca	ttt	gct	tca	aat	gaa	tcc	att	aaa	ggg	caa	qtc	gaa	gct	gtt	aaa	654
77	Pro	Phe	Ala	Ser	Asn	Glu	Ser	Ile	Lys	Gly	Gln	Val	Glu	Ala	Val	Lys	
78							155			160			165				
80	caa	gtg	caa	gcg	act	gtg	ctt	acc	tat	ccc	gat	ttg	cag	cct	acg	gat	702
81	Gln	Val	Gln	Ala	Thr	Val	Leu	Thr	Tyr	Pro	Asp	Leu	Gln	Pro	Thr	Asp	
82			170				175				180						
84	aga	gca	act	att	tac	gtt	aaa	tca	aaa	tta	gac	aag	ctt	att	tgg	caa	750
85	Arg	Ala	Thr	Ile	Tyr	Val	Lys	Ser	Lys	Leu	Asp	Lys	Leu	Ile	Trp	Gln	
86			185				190				195						
88	aca	aga	att	acc	aga	gat	caa	aaa	gtt	ctt	aat	gta	aag	agt	ttt	gaa	798
89	Thr	Arg	Ile	Thr	Arg	Asp	Gln	Lys	Val	Leu	Asn	Val	Lys	Ser	Phe	Glu	
90			200				205				210						
92	gtt	tat	cat	caa	tta	aat	aaa	gtc	aca	cat	gca	gtt	gtt	gtt	gtt	caa	846
93	Val	Tyr	His	Gln	Leu	Asn	Lys	Ala	Ile	Thr	His	Ala	Val	Gly	Val	Gln	
94			215				220				225				230		
96	tta	aat	cca	act	gta	aca	gtt	gca	caa	gtt	gac	caa	gaa	atc	aaa	gtg	894
97	Leu	Asn	Pro	Thr	Val	Thr	Val	Ala	Gln	Val	Asp	Gln	Glu	Ile	Lys	Val	
98							235			240			245				
100	cta	caa	gaa	gca	tta	aat	act	gtc	cta	cag	taaggtagag	attqaattqa					944
101	Leu	Gln	Glu	Ala	Leu	Asn	Thr	Ala	Leu	Gln							
102			250				255										
104	cgtattaaaa	aggactggaa	tttattaatt	ttagtcctt	agaattttta	tttagctgtat											1004
106	ttacttgtt	aaagagattt	gtggaaaata	aagtaccata	tttcattttct	cctccaaata											1064
108	tttgttatqtc	gattcccttc	taaaacataq	ctaattatgtt	tagttttctq	gctaataqat											1124
110	tgtacatqaa	atttgtcaaa	attactaqqq	taaaaggttt	ttctttttat	aaatccatca											1184
112	tgactat																1191
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116	-211	LENGTH:	256														
117	-212	TYPE:	PR														
118	-213	ORGANISM:	Artificial Sequence														
119	-220	FEATURE															
121	<223>	OTHER INFORMATION	Description of Artificial Sequence	CAMP factor													
122		preprotein															
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125	Met	Glu	Phe	Lys	Lys	Leu	Leu	Tyr	Leu	Thr	Gly	Ser	Ile	Ala	Gly	Ile	
126						5				10			15				
128	Thr	Leu	Phe	Ser	Pro	Ile	Leu	Thr	Ser	Val	Gln	Ala	Asn	Gln	Ile	Asn	

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134	Glu	Glu	Ile	Asp	Asn	Ser	Leu	Asn	Gln	Glu	Ser	Ala	Gln	Leu	Tyr	Ala
135	50						55					60				
137	Leu	Lys	Glu	Asp	Val	Lys	Gly	Thr	Glu	Lys	Glu	Gln	Ser	Val	Asn	Ser
138	65						70				75				80	
140	Ala	Ile	Ser	Ala	Val	Glu	Asn	Leu	Lys	Thr	Ser	Leu	Arg	Ala	Asn	Pro
141							85				90			95		
143	Glu	Ihr	Ile	Tyr	Asp	Leu	Asn	Ser	Ile	Gly	Thr	Arg	Val	Glu	Ala	Ile
144							100			105			110			
146	Ser	Asp	Val	Ile	Gln	Ala	Ile	Val	Phe	Ser	Thr	Gln	Gln	Leu	Thr	Asn
147							115			120			125			
149	Lys	Val	Asp	Gln	Ala	His	Ile	Asp	Met	Gly	Phe	Ala	Ile	Thr	Lys	Leu
150	130						135				140					
152	Leu	Ile	Arg	Ile	Ala	Asp	Pro	Phe	Ala	Ser	Asn	Glu	Ser	Ile	Lys	Gly
153	145						150				155			160		
155	Gln	Val	Glu	Ala	Val	Lys	Gln	Val	Gln	Ala	Thr	Val	Leu	Thr	Tyr	Pro
156							165			170			175			
158	Asp	Leu	Gln	Pro	Thr	Asp	Arg	Ala	Thr	Ile	Tyr	Val	Lys	Ser	Lys	Leu
159							180			185			190			
161	Asp	Lys	Leu	Ile	Trp	Gln	Thr	Arg	Ile	Thr	Arg	Asp	Gln	Lys	Val	Leu
162							195			200			205			
164	Asn	Val	Lys	Ser	Phe	Glu	Val	Tyr	His	Gln	Leu	Asn	Lys	Ala	Ile	Thr
165	210						215				220					
167	His	Ala	Val	Gly	Val	Gln	Leu	Asn	Pro	Thr	Val	Thr	Val	Ala	Gln	Val
168	225						230				235			240		
170	Asp	Gln	Glu	Ile	Lys	Val	Leu	Gln	Glu	Ala	Leu	Asn	Thr	Ala	Leu	Gln
171							245			250			255			
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175	<211>	LENGTH:	256													
176	<212>	TYPE:	PRT													
177	<213>	ORGANISM:	Artificial Sequence													
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181		CAMP	factor protein													
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185	1						5			10			15			
187	Ihr	Ieu	Phe	Ser	Pro	Ile	Ieu	Thr	Ser	Val	Gln	Ala	Asn	Gln	Ile	Asn
188							20			25			30			
190	Val	Ser	Gln	Pro	Ser	Asn	Asn	Glu	Ser	Asn	Val	Ile	Ser	Gln	Lys	Iys
191							35			40			45			
193	Glu	Glu	Ile	Asp	Asn	Ser	Leu	Asn	Gln	Glu	Ser	Ala	Gln	Leu	Tyr	Ala
194	50						55				60					
196	Leu	Lys	Glu	Asp	Val	Lys	Gly	Thr	Glu	Lys	Glu	Gln	Ser	Val	Asn	Ser
197	65						70			75			80			
199	Ala	Ile	Ser	Ala	Val	Glu	Asn	Ieu	Lys	Thr	Ser	Ieu	Arg	Ala	Asn	Pro
200							85			90			95			

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206	115	120	125	
208	Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala Ile Thr Lys Leu			
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211	Leu Ile Arg Ile Ala Asp Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly			
212	145	150	155	160
214	Gln Val Glu Ala Val Lys Gln Val Gln Ala Thr Val Leu Thr Tyr Pro			
215	165	170	175	
217	Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu			
218	180	185	190	
220	Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp Gln Lys Val Leu			
221	195	200	205	
223	Asn Val Lys Ser Phe Glu Val Tyr His Gln Leu Asn Lys Ala Ile Thr			
224	210	215	220	
226	His Ala Val Gly Val Gln Leu Asn Pro Thr Val Thr Val Ala Gln Val			
227	225	230	235	240
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230	245	250	255	
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237	<211> LENGTH: 226			
238	<212> TYPE: PRT			
239	<213> ORGANISM: Artificial Sequence			
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242	<223> OTHER INFORMATION: Description of Artificial Sequence: S. agalactiae			
243	CAMP factor protein			
245	<400> SEQUENCE: 4			
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247	1	5	10	15
249	Gln Ala Gln Gln Met Ala Gln Lys Leu Asp Gln Asp Ser Ile Gln Leu			
250	20	25	30	
252	Arg Asn Ile Lys Asp Asn Val Gln Gly Thr Asp Tyr Glu Lys Pro Val			
253	35	40	45	
255	Asn Glu Ala Ile Thr Ser Val Glu Lys Leu Lys Thr Ser Leu Arg Ala			
256	50	55	60	
258	Asn Ser Glu Thr Val Tyr Asp Leu Asn Ser Ile Gly Ser Arg Val Glu			
259	65	70	75	80
261	Ala Leu Thr Asp Val Ile Glu Ala Ile Thr Phe Ser Thr Gln His Leu			
262	85	90	95	
264	Ala Asn Lys Val Ser Gln Ala Asn Ile Asp Met Gln Phe Gly Ile Thr			
265	100	105	110	
267	Lys Leu Val Ile Arg Ile Leu Asp Pro Phe Ala Ser Val Asp Ser Ile			
268	115	120	125	
270	Lys Ala Gln Val Asn Asp Val Lys Ala Leu Glu Gln Lys Val Leu Thr			
271	130	135	140	
273	Tyr Pro Asp Leu Lys Pro Thr Asp Arg Ala Thr Ile Tyr Thr Lys Ser			
274	145	150	155	160
276	Ile Asp Arg Ile Asp Ile Asp Asn Thr Asp Phe Asp Ile Asp Ile Asp			

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282 Ile Thr His Ala Val Gly Val Gln Leu Asn Pro Asn Val Thr Val Gln
 283 195 200 205
 285 Gln Val Asp Gln Glu Ile Val Thr Leu Gln Ala Ala Leu Gln Thr Ala
 286 210 215 220
 288 Leu Lys
 289 225
 292 <210> SEQ ID NO: 5
 293 <211> LENGTH: 228
 294 <212> TYPE: PRT
 295 <213> ORGANISM: Artificial Sequence
 297 <220> FEATURE:
 298 <223> OTHER INFORMATION: Description of Artificial Sequence: mature S. uberis
 299 CAMP factor protein
 301 <400> SEQUENCE: 5
 302 Asn Gln Ile Asn Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile
 303 1 5 10 15
 305 Ser Gln Lys Lys Glu Glu Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala
 306 20 25 30
 308 Gln Leu Tyr Ala Leu Lys Glu Asp Val Lys Gly Thr Glu Lys Glu Gln
 309 35 40 45
 311 Ser Val Asn Ser Ala Ile Ser Ala Val Glu Asn Leu Lys Thr Ser Leu
 312 50 55 60
 314 Arg Ala Asn Pro Glu Thr Ile Tyr Asp Leu Asn Ser Ile Gly Thr Arg
 315 65 70 75 80
 317 Val Glu Ala Ile Ser Asp Val Ile Gln Ala Ile Val Phe Ser Thr Gln
 318 85 90 95
 320 Gln Leu Thr Asn Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala
 321 100 105 110
 323 Ile Thr Lys Leu Leu Ile Arg Ile Ala Asp Pro Phe Ala Ser Asn Glu
 324 115 120 125
 326 Ser Ile Lys Gly Gln Val Glu Ala Val Lys Gln Val Gln Ala Thr Val
 327 130 135 140
 329 Leu Thr Tyr Pro Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val
 330 145 150 155 160
 332 Lys Ser Lys Leu Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp
 333 165 170 175
 335 Gln Lys Val Leu Asn Val Lys Ser Phe Glu Val Tyr His Gln Leu Asn
 336 180 185 190
 338 Lys Ala Ile Thr His Ala Val Gly Val Gln Leu Asn Pro Thr Val Thr
 339 195 200 205
 341 Val Ala Gln Val Asp Gln Glu Ile Lys Val Leu Gln Glu Ala Leu Asn
 342 210 215 220
 344 Thr Ala Leu Gln
 345 225

VERIFICATION SUMMARY

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